

initiating transcription of the cDNA or DNA to double stranded (ds) RNA upon binding of an appropriate transcription factor to the promoter(s), b) introducing said library into one or more of the cells comprising the transcription factor, and c) identifying and isolating a particular phenotype of the cell comprising the library and identifying the DNA or cDNA fragment from the library responsible for conferring the phenotype. Using this technique it is also possible to assign function to a known DNA sequence by a) identifying a homologue(s) of the DNA sequence in a cell, b) isolating the relevant DNA homologue(s) or a fragment thereof from the cell, c) cloning the homologue or fragment thereof into an appropriate vector in an orientation relative to a suitable promoter(s) capable of initiating transcription of dsRNA from the DNA homologue or fragment upon binding of an appropriate transcription factor to the promoter(s), and d) introducing the vector into the cell from step a) comprising the transcription factor.

In the Claims

Please amend the claims as follows. Applicants have included herewith pages showing the markups of the claims with insertions and deletions indicated by underlining and bracketing, respectively.

- 1.(amended) A method of identifying DNA responsible for conferring a phenotype of a nematode cell or organism, which method comprises
- a) constructing a cDNA or genomic library of the DNA of said nematode cell or organism in a vector in an orientation relative to a promoter(s) that initiates transcription of said cDNA or DNA to double stranded (ds) RNA upon binding of a transcription factor to said promoter(s),
 - b) introducing said library into one or more of said nematode cells or organisms comprising said transcription factor, and
 - c) identifying a phenotype of said nematode cell or organism comprising said library and identifying the DNA or cDNA fragment from said library responsible for conferring said phenotype.

- 3.(amended) A method of assigning function to a known DNA sequence which method comprises

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CONT.
- a) identifying a homologue(s) of said known DNA sequence in a nematode cell or organism,
 - b) isolating the relevant DNA homologue(s) or a fragment thereof from said nematode cell or organism,
 - c) cloning said homologue or fragment thereof into a vector in an orientation relative to a promoter(s) that initiates transcription of dsRNA from said DNA homologue or fragment upon binding of a transcription factor to said promoter(s),
 - d) introducing said vector into said nematode cell or organism from step a) comprising said transcription factor, and
 - e) identifying the phenotype of said nematode cell or organism compared to wild type.
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D3

7.(twice amended) A method according to any of claims 1 or 3 wherein said DNA library, homologue or fragment is constructed in a vector which comprises a sequence of nucleotides encoding said transcription factor operably linked to a promoter.

8.(twice amended) A method according to any of claims 1 or 3 wherein said transcription factor is encoded by a further vector independent of the vector including said DNA library, DNA homologue or fragment and which sequence encoding said transcription factor is operably linked to a promoter.

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10.(twice amended) A method according to claim 7 wherein said promoter comprises any of let 858, SERCA, UL6, myo-2 or myo-3.

11.(twice amended) A method according to claim 7, wherein said vector comprises a selectable marker.

12.(amended) A method according to claim 11 wherein said selectable marker comprises a nucleotide sequence capable of inhibiting or preventing expression of a gene in said nematode cell and which gene is responsible for conferring a phenotype.

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D4
13.(amended) A method according to claim 12 wherein said nucleotide sequence comprises a sequence which is a part of or identical to said gene conferring said phenotype, and which nucleotide sequence is itself oriented relative to a promoter(s) that initiates transcription of double stranded RNA upon binding of a transcription factor to said promoter(s).

CONT.
14.(amended) A method according to claim 12 wherein said nucleotide sequence is a part of or identical to said gene sequence conferring said phenotype, and which nucleotide sequence is such as to permit integration of said vector by homologous recombination in the genome of said nematode cell or organism and following said integration said nucleotide sequence is capable of inhibiting expression of said gene sequence conferring said phenotype.

D5
20.(twice amended) A method according to any of claims 1 or 3 wherein said nematode cell or organism is contacted with a specified compound for screening for a desired phenotype.

38.(amended) A method of validating clones identified in yeast two hybrid vector experiments which method comprises

D6
a) providing a construct including the DNA encoding the protein identified in the two hybrid vector experiment, which construct is such that said DNA is orientated relative to a promoter(s) that initiates transcription of said DNA to double stranded RNA upon binding of a transcription factor to said promoter(s),

b) transforming a nematode cell or organism comprising said transcription factor with said construct, and

c) identifying a phenotypic change in said nematode cell or organism when compared to a wild type.

D7
48.(amended) A method according to claim 47 wherein said organism is of the species *C. elegans*.

Please add the following new claim: